



36120A Suppl SL
SEQUENCE LISTING

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Frischauf, Anna Maria

<120> METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND NUCLEIC
ACIDS

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<140> 09/905,744

<141> 2001-07-13

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<170> PatentIn version 3.1

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aaaacgagct acatttttca gcagccgcag cacggtcctt ggcaaacaag g atg aga	237
	Met Arg 1
aaa ata tcc aac cac ggg agc ctg cgg gtg gcg aag gtg gca tac ccc	285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro	
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Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp	
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cac cgg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc	381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala	
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Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala	
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gca gac ggg cac gag gtc ttc tac ggg atc atg ttt gat gca gga agc	477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser	
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act ggc acc cga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa	525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	
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act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt	573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	
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Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	
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Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	
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Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala	
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Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr	
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gat gaa ggc gtt tcg gcg tgg atc acc atc aac ttc ctg aca ggc agc	861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
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Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	
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Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr	
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Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala	
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Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly	
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Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp	
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Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe	
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Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu	
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Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro	
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Gln Lys Ser Pro Ala Ser	
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Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
20          25          30

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Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
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Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
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Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala
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Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
85 90 95

Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
100 105 110

Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
115 120 125

Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
130 135 140

Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
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Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
165 170 175

Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn
180 185 190

Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
195 200 205

Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
210 215 220

Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
225 230 235 240

Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
245 250 255

Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
260 265 270

Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
275 280 285

Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
290 295 300

Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
305 310 315 320

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Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
 325 330 335

Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
 340 345 350

Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
 355 360 365

Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
 370 375 380

Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
 385 390 395 400

Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly
 405 410 415

Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val
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 Met Phe Thr Val Leu Thr Arg Gln Pro Cys

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Leu	Val	Val	Leu	Leu	Val	Ser	Ile	Val	Val	Leu	Val	Ser	Ile	Thr	Val	
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Ile	Gln	Ile	His	Lys	Gln	Glu	Val	Leu	Pro	Pro	Gly	Leu	Lys	Tyr	Gly	
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Ile	Val	Leu	Asp	Ala	Gly	Ser	Ser	Arg	Thr	Thr	Val	Tyr	Val	Tyr	Gln	
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Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asn	Thr	Gly	Val	Val	Ser	Gln	Thr	Phe	
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Gln	Asp	Val	Pro	Arg	Ala	Phe	Glu	Glu	Cys	Met	Gln	Lys	Val	Lys	Gly	
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Gln	Val	Pro	Ser	His	Leu	His	Gly	Ser	Thr	Pro	Ile	His	Leu	Gly	Ala	
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Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Leu	Gln	Asn	Glu	Thr	Ala	Ala	Asn	
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Phe	Arg	Gly	Ala	Gln	Ile	Ile	Ser	Gly	Gln	Glu	Glu	Gly	Val	Tyr	Gly	
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Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Ile	Ser	Phe	Val	Ala	Gly	Glu	Lys	
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atg	gat	ctg	aac	acc	agc	gac	atc	atg	cag	gtg	tcc	ctg	tat	ggc	tac	832
Met	Asp	Leu	Asn	Thr	Ser	Asp	Ile	Met	Gln	Val	Ser	Leu	Tyr	Gly	Tyr	
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 Asp His Ala Val Asp Ser Asp
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Ser Ile Val Val Leu Val Ser Ile Thr Val Ile Gln Ile His Lys Gln
35 40 45

Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly Ile Val Leu Asp Ala Gly
50 55 60

Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln Trp Pro Ala Glu Lys Glu
65 70 75 80

Asn Asn Thr Gly Val Val Ser Gln Thr Phe Lys Cys Ser Val Lys Gly
85 90 95

Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro Gln Asp Val Pro Arg Ala
100 105 110

Phe Glu Glu Cys Met Gln Lys Val Lys Gly Gln Val Pro Ser His Leu
115 120 125

His Gly Ser Thr Pro Ile His Leu Gly Ala Thr Ala Gly Met Arg Leu
130 135 140

Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn Glu Val Leu Glu Ser Ile
145 150 155 160

Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp Phe Arg Gly Ala Gln Ile
165 170 175

Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly Trp Ile Thr Ala Asn Tyr
180 185 190

Leu Met Gly Asn Phe Leu Glu Lys Asn Leu Trp His Met Trp Val His
195 200 205

Pro His Gly Val Glu Thr Thr Gly Ala Leu Asp Leu Gly Gly Ala Ser
210 215 220

Thr Gln Ile Ser Phe Val Ala Gly Glu Lys Met Asp Leu Asn Thr Ser
225 230 235 240

Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr Val Tyr Thr Leu Tyr Thr
245 250 255

His Ser Phe Gln Cys Tyr Gly Arg Asn Glu Ala Glu Lys Lys Phe Leu
260 265 270

36120A Suppl SL

Ala Met Leu Leu Gln Asn Ser Pro Thr Lys Asn His Leu Thr Asn Pro
275 280 285

Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe Thr Met Gly His Val Phe
290 295 300

Asp Ser Leu Cys Thr Val Asp Gln Arg Pro Glu Ser Tyr Asn Pro Asn
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Asp Val Ile Thr Phe Glu Gly Thr Gly Asp Pro Ser Leu Cys Lys Glu
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Lys Val Ala Ser Ile Phe Asp Phe Lys Ala Cys His Asp Gln Glu Thr
340 345 350

Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys Ile Lys Gly Pro Phe Val
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Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser Ala Leu Asn Leu Ser Gly
370 375 380

Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser Thr Trp Asn Phe Cys Ser
385 390 395 400

Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu Pro Lys Phe Asp Glu Val
405 410 415

Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn Tyr Ile Tyr His Leu Phe
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Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr Trp Pro Gln Ile His Phe
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Glu Lys Glu Val Gly Asn Ser Ser Ile Ala Trp Ser Leu Gly Tyr Met
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Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu Ser Pro Leu Ile Arg Leu
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Pro Ile Glu Pro Pro Val Phe Val Gly Thr Leu Ala Phe Phe Thr Val
485 490 495

Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala Tyr Leu Cys Ser Ala Thr
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36120A Suppl SL

Asp

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tgcaggtgtg cgagcaggat tgcttctgca acaaaaagcct ccacccagcc acatcttggg      240
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Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe
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Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile
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36120A Suppl SL

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Val	Pro	Lys	Gly	Ser	Val	Ser	Ile	Met	Asp	Gly	Ser	Asp	Glu	Gly	Ile	
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Arg	Gln	Glu	Thr	Val	Gly	Thr	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	
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Ile	Thr	Phe	Leu	Pro	Gln	Phe	Glu	Lys	Thr	Leu	Glu	Gln	Thr	Pro	Arg	
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Thr	His	Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	Arg	Leu	Ala	Thr	
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Lys	Tyr	Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Val	Gly	Phe	Glu	Pro	
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Cys	Tyr	Ala	Glu	Val	Leu	Arg	Val	Val	Arg	Gly	Lys	Leu	His	Gln	Pro	
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Glu	Glu	Val	Gln	Arg	Gly	Ser	Phe	Tyr	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	
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cga	gct	gtt	gac	aca	gac	atg	att	gat	tat	gaa	aag	ggg	ggt	att	tta	1296
Arg	Ala	Val	Asp	Thr	Asp	Met	Ile	Asp	Tyr	Glu	Lys	Gly	Gly	Ile	Leu	
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Lys	Val	Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	Cys	Asp	Asn	Leu	
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36120A suppl SL

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Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val	
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tta cag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg	1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu	
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Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His	
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Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
50 55 60
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly

36120A Suppl SL
75

65

70

80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
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Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
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130 135 140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
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Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
165 170 175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
180 185 190

Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
195 200 205

Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
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Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
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Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
245 250 255

Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
260 265 270

Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
275 280 285

Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
290 295 300

Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305 310 315 320

36120A Suppl SL
val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
325 330 335

Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
340 345 350

Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
355 360 365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
370 375 380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
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tcaggtccac atcttgggaa gaat atg gcc act tcc tgg ggg gct gtc ttc 231
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Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
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36120A Suppl SL

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Val	Ser	Ala	Gly	Thr	Phe	Tyr	Gly	Ile	Met	Phe	Asp	Ala	Gly	Ser	Thr	
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Gly	Ala	Arg	Ile	His	Val	Tyr	Thr	Phe	Val	Gln	Lys	Thr	Ala	Gly	Gln	
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Leu	Pro	Phe	Leu	Glu	Gly	Glu	Ile	Phe	Asp	Ser	Val	Lys	Pro	Gly	Leu	
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Leu	Leu	Glu	Val	Ala	Lys	Asp	Ser	Ile	Pro	Arg	Ser	His	Trp	Glu	Arg	
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Gln	Lys	Ala	Gln	Ala	Leu	Leu	Leu	Glu	Val	Glu	Glu	Ile	Phe	Lys	Asn	
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Tyr	Glu	Gly	Ile	Leu	Ala	Trp	Val	Thr	Val	Asn	Phe	Leu	Thr	Gly	Gln	
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Ala	Ser	Thr	Gln	Ile	Thr	Phe	Leu	Pro	Gln	Phe	Glu	Lys	Thr	Leu	Glu	
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Gln	Thr	Pro	Arg	Gly	Tyr	Leu	Thr	Ser	Phe	Glu	Met	Phe	Asn	Ser	Thr	
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Phe	Lys	Leu	Tyr	Thr	His	Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	
	235					240					245					
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Arg	Leu	Ala	Thr	Leu	Gly	Ala	Leu	Glu	Ala	Lys	Gly	Thr	Asp	Gly	His	
				255					260						265	
acg	ttt	cga	agt	gcc	tgt	tta	cca	aga	tgg	ttg	gaa	gca	gag	tgg	atc	1047
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36120A Suppl SL

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Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys	
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Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser	
315 320 325	
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Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys	
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Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val	
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Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met	
365 370 375	
gac ctc act tac atc aca gcc ctg ttg aaa gat ggt ttg ggc ttt gcc	1383
Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala	
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410 415 420 425	
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His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro	
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Gly Lys Ala Trp Pro Glu Thr Arg	
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36120A Suppl SL

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 35 40 45

Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Ala Arg Ile His Val Tyr
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Thr Phe Val Gln Lys Thr Ala Gly Gln Leu Pro Phe Leu Glu Gly Glu
 65 70 75 80

Ile Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln Pro
 85 90 95

Lys Gln Gly Ala Glu Thr Val Gln Glu Leu Leu Glu Val Ala Lys Asp
 100 105 110

Ser Ile Pro Arg Ser His Trp Glu Arg Thr Pro Val Val Leu Lys Ala
 115 120 125

Thr Ala Gly Leu Arg Leu Leu Pro Glu Gln Lys Ala Gln Ala Leu Leu
 130 135 140

Leu Glu Val Glu Glu Ile Phe Lys Asn Ser Pro Phe Leu Val Pro Asp
 145 150 155 160

Gly Ser Val Ser Ile Met Asp Gly Ser Tyr Glu Gly Ile Leu Ala Trp
 165 170 175

Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly Arg Gly Gln Glu
 180 185 190

36120A Suppl SL

Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr Phe
195 200 205

Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr Leu
210 215 220

Thr Ser Phe Glu Met Phe Asn Ser Thr Phe Lys Leu Tyr Thr His Ser
225 230 235 240

Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly Ala
245 250 255

Leu Glu Ala Lys Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys Leu
260 265 270

Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr Gln
275 280 285

Tyr Gly Gly Asn Gln Glu Gly Glu Met Gly Phe Glu Pro Cys Tyr Ala
290 295 300

Glu Val Leu Arg Val Val Gln Gly Lys Leu His Gln Pro Glu Glu Val
305 310 315 320

Arg Gly Ser Ala Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala Ala
325 330 335

Asp Thr His Leu Ile Asp Tyr Glu Lys Gly Gly Val Leu Lys Val Glu
340 345 350

Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Gly Ser Phe
355 360 365

Ser Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Thr Tyr Ile Thr Ala
370 375 380

Leu Leu Lys Asp Gly Leu Gly Phe Ala Glu Arg His Pro Leu Thr Ala
385 390 395 400

His Lys Glu Ser Glu Gln His Arg Asp Trp Leu Gly Leu Gly Gly His
405 410 415

Leu Ser Pro Ala Pro Val Ser Gly His His Gln Leu Arg Pro Ser Ser
420 425 430

Thr Ser Glu Ala Cys Ile Ser Glu Pro Val Phe Ser Gln Glu Gly Val

435

440

36120A Suppl SL
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Arg
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<213> Homo sapiens

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 35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
 50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
 85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
 100 105 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
 115 120 125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
 130 135 140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
 145 150 155 160

36120A suppl SL

Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
 165 170 175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
 180 185 190

Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
 195 200 205

Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
 210 215 220

Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
 225 230 235 240

Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
 245 250 255

Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
 260 265 270

Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
 275 280 285

Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
 290 295 300

Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
 305 310 315 320

Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
 325 330 335

Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
 340 345 350

Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
 355 360 365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
 370 375 380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
 385 390 395 400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
 405 410 415

36120A Suppl SL

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
420 425

<210> 10

<211> 455

<212> PRT

<213> P. sativum

<400> 10

Met Glu Leu Leu Ile Lys Leu Ile Thr Phe Leu Leu Phe Ser Met Pro
1 5 10 15

Ala Ile Thr Ser Ser Gln Tyr Leu Gly Asn Asn Leu Leu Thr Ser Arg
20 25 30

Lys Ile Phe Leu Lys Gln Glu Glu Ile Ser Ser Tyr Ala Val Val Phe
35 40 45

Asp Ala Gly Ser Thr Gly Ser Arg Ile His Val Tyr His Phe Asn Gln
50 55 60

Asn Leu Asp Leu Leu His Ile Gly Lys Gly Val Glu Tyr Tyr Asn Lys
65 70 75 80

Ile Thr Pro Gly Leu Ser Ser Tyr Ala Asn Asn Pro Glu Gln Ala Ala
85 90 95

Lys Ser Leu Ile Pro Leu Leu Glu Gln Ala Glu Asp Val Val Pro Asp
100 105 110

Asp Leu Gln Pro Lys Thr Pro Val Arg Leu Gly Ala Thr Ala Gly Leu
115 120 125

Arg Leu Leu Asn Gly Asp Ala Ser Glu Lys Ile Leu Gln Ser Val Arg
130 135 140

Asp Met Leu Ser Asn Arg Ser Thr Phe Asn Val Gln Pro Asp Ala Val
145 150 155 160

Ser Ile Ile Asp Gly Thr Gln Glu Gly Ser Tyr Leu Trp Val Thr Val
165 170 175

Asn Tyr Ala Leu Gly Asn Leu Gly Lys Lys Tyr Thr Lys Thr Val Gly
180 185 190

36120A Suppl SL

Val Ile Asp Leu Gly Gly Gly Ser Val Gln Met Ala Tyr Ala Val Ser
195 200 205

Lys Lys Thr Ala Lys Asn Ala Pro Lys Val Ala Asp Gly Asp Asp Pro
210 215 220

Tyr Ile Lys Lys Val Val Leu Lys Gly Ile Pro Tyr Asp Leu Tyr Val
225 230 235 240

His Ser Tyr Leu His Phe Gly Arg Glu Ala Ser Arg Ala Glu Ile Leu
245 250 255

Lys Leu Thr Pro Arg Ser Pro Asn Pro Cys Leu Leu Ala Gly Phe Asn
260 265 270

Gly Ile Tyr Thr Tyr Ser Gly Glu Glu Phe Lys Ala Thr Ala Tyr Thr
275 280 285

Ser Gly Ala Asn Phe Asn Lys Cys Lys Asn Thr Ile Arg Lys Ala Leu
290 295 300

Lys Leu Asn Tyr Pro Cys Pro Tyr Gln Asn Cys Thr Phe Gly Gly Ile
305 310 315 320

Trp Asn Gly Gly Gly Gly Asn Gly Gln Lys Asn Leu Phe Ala Ser Ser
325 330 335

Ser Phe Phe Tyr Leu Pro Glu Asp Thr Gly Met Val Asp Ala Ser Thr
340 345 350

Pro Asn Phe Ile Leu Arg Pro Val Asp Ile Glu Thr Lys Ala Lys Glu
355 360 365

Ala Cys Ala Leu Asn Phe Glu Asp Ala Lys Ser Thr Tyr Pro Phe Leu
370 375 380

Asp Lys Lys Asn Val Ala Ser Tyr Val Cys Met Asp Leu Ile Tyr Gln
385 390 395 400

Tyr Val Leu Leu Val Asp Gly Phe Gly Leu Asp Pro Leu Gln Lys Ile
405 410 415

Thr Ser Gly Lys Glu Ile Glu Tyr Gln Asp Ala Ile Val Glu Ala Ala
420 425 430

Trp Pro Leu Gly Asn Ala Val Glu Ala Ile Ser Ala Leu Pro Lys Phe

435

440

445

Glu Arg Leu Met Tyr Phe Val
450 455

<210> 11

<211> 454

<212> PRT

<213> Solanum tuberosum

<400> 11

Met Leu Asn Gln Asn Ser His Phe Ile Phe Ile Ile Leu Ala Ile Phe
1 5 10 15

Leu Val Leu Pro Leu Ser Leu Leu Ser Lys Asn Val Asn Ala Gln Ile
20 25 30

Pro Leu Arg Arg His Leu Leu Ser His Glu Ser Glu His Tyr Ala Val
35 40 45

Ile Phe Asp Ala Gly Ser Thr Gly Ser Arg Val His Val Phe Arg Phe
50 55 60

Asp Glu Lys Leu Gly Leu Leu Pro Ile Gly Asn Asn Ile Glu Tyr Phe
65 70 75 80

Met Ala Thr Glu Pro Gly Leu Ser Ser Tyr Ala Glu Asp Pro Lys Ala
85 90 95

Ala Ala Asn Ser Leu Glu Pro Leu Leu Asp Gly Ala Glu Gly Val Val
100 105 110

Pro Gln Glu Leu Gln Ser Glu Thr Pro Leu Glu Leu Gly Ala Thr Ala
115 120 125

Gly Leu Arg Met Leu Lys Gly Asp Ala Ala Glu Lys Ile Leu Gln Ala
130 135 140

Val Arg Asn Leu Val Lys Asn Gln Ser Thr Phe His Ser Lys Asp Gln
145 150 155 160

Trp Val Thr Ile Leu Asp Gly Thr Gln Glu Gly Ser Tyr Met Trp Ala
165 170 175

36120A Suppl SL

Ala Ile Asn Tyr Leu Leu Gly Asn Leu Gly Lys Asp Tyr Lys Ser Thr
 180 185 190

Thr Ala Thr Ile Asp Leu Gly Gly Gly Ser Val Gln Met Ala Tyr Ala
 195 200 205

Ile Ser Asn Glu Gln Phe Ala Lys Ala Pro Gln Asn Glu Asp Gly Glu
 210 215 220

Pro Tyr Val Gln Gln Lys His Leu Met Ser Lys Asp Tyr Asn Leu Tyr
 225 230 235 240

Val His Ser Tyr Leu Asn Tyr Gly Gln Leu Ala Gly Arg Ala Glu Ile
 245 250 255

Phe Lys Ala Ser Arg Asn Glu Ser Asn Pro Cys Ala Leu Glu Gly Cys
 260 265 270

Asp Gly Tyr Tyr Ser Tyr Gly Gly Val Asp Tyr Lys Val Lys Ala Pro
 275 280 285

Lys Lys Gly Ser Ser Trp Lys Arg Cys Arg Arg Leu Thr Arg His Ala
 290 295 300

Leu Lys Ile Asn Ala Lys Cys Asn Ile Glu Glu Cys Thr Phe Asn Gly
 305 310 315 320

Val Trp Asn Gly Gly Gly Gly Asp Gly Gln Lys Asn Ile His Ala Ser
 325 330 335

Ser Phe Phe Tyr Asp Ile Gly Ala Gln Val Gly Ile Val Asp Thr Lys
 340 345 350

Phe Pro Ser Ala Leu Ala Lys Pro Ile Gln Tyr Leu Asn Ala Ala Lys
 355 360 365

Val Ala Cys Gln Thr Asn Val Ala Asp Ile Lys Ser Ile Phe Pro Lys
 370 375 380

Thr Gln Asp Arg Asn Ile Pro Tyr Leu Cys Met Asp Leu Ile Tyr Glu
 385 390 395 400

Tyr Thr Leu Leu Val Asp Gly Phe Gly Leu Asn Pro His Lys Glu Ile
 405 410 415

Thr Val Ile His Asp Val Gln Tyr Lys Asn Tyr Leu Val Gly Ala Ala
 420 425 430

36120A Suppl SL

Trp Pro Leu Gly Cys Ala Ile Asp Leu Val Ser Ser Thr Thr Asn Lys
435 440 445

Ile Arg Val Ala Ser Ser
450

<210> 12

<211> 473

<212> PRT

<213> Saccharomyces cerevisiae

<400> 12

Lys Thr Pro Glu Asp Ile Ser Ile Ile Pro Val Asn Asp Glu Pro Gly
1 5 10 15

Tyr Leu Gln Asp Ser Lys Thr Glu Gln Asn Tyr Pro Glu Leu Ala Asp
20 25 30

Ala Val Lys Ser Gln Thr Ser Gln Thr Cys Ser Glu Glu His Lys Tyr
35 40 45

Val Ile Met Ile Asp Ala Gly Ser Thr Gly Ser Arg Val His Ile Tyr
50 55 60

Lys Phe Asp Val Cys Thr Ser Pro Pro Thr Leu Leu Asp Glu Lys Phe
65 70 75 80

Asp Met Leu Glu Pro Gly Leu Ser Ser Phe Asp Thr Asp Ser Val Gly
85 90 95

Ala Ala Asn Ser Leu Asp Pro Leu Leu Lys Val Ala Met Asn Tyr Val
100 105 110

Pro Ile Lys Ala Arg Ser Cys Thr Pro Val Ala Val Lys Ala Thr Ala
115 120 125

Gly Leu Arg Leu Leu Gly Asp Ala Lys Ser Ser Lys Ile Leu Ser Ala
130 135 140

Val Arg Asp His Leu Glu Lys Asp Tyr Pro Phe Pro Val Val Glu Gly
145 150 155 160

Asp Gly Val Ser Ile Met Gly Gly Asp Glu Glu Gly Val Phe Ala Trp
165 170 175

36120A Suppl SL

Ile Thr Thr Asn Tyr Leu Leu Gly Asn Ile Gly Ala Asn Gly Pro Lys
180 185 190

Leu Pro Thr Ala Ala Val Phe Asp Leu Gly Gly Gly Ser Thr Gln Ile
195 200 205

Val Glu Glu Pro Thr Phe Pro Ile Asn Glu Lys Met Val Asp Gly Glu
210 215 220

His Lys Phe Asp Leu Lys Phe Gly Asp Glu Asn Tyr Thr Leu Tyr Gln
225 230 235 240

Phe Ser His Leu Gly Tyr Gly Leu Lys Glu Gly Arg Asn Lys Val Asn
245 250 255

Ser Val Leu Val Glu Asn Ala Leu Lys Asp Lys Ile Leu Lys Gly Cys
260 265 270

Asn Thr Lys Thr His Cys Leu Ser Ser Pro Cys Leu Pro Pro Lys Val
275 280 285

Asn Ala Thr Asn Glu Lys Val Thr Leu Glu Ser Lys Glu Thr Tyr Thr
290 295 300

Ile Asp Phe Ile Gly Pro Asp Glu Pro Ser Gly Ala Gln Cys Arg Phe
305 310 315 320

Leu Thr Asp Glu Ile Leu Asn Lys Asp Ala Gln Cys Gln Ser Pro Pro
325 330 335

Cys Ser Phe Asn Gly Val His Gln Pro Ser Leu Val Arg Thr Phe Lys
340 345 350

Glu Ser Asn Asp Ile Tyr Ile Phe Ser Tyr Phe Tyr Asp Arg Thr Thr
355 360 365

Arg Pro Leu Gly Met Pro Leu Ser Phe Thr Leu Asn Glu Leu Asn Asp
370 375 380

Leu Ala Arg Ile Val Cys Lys Gly Glu Glu Thr Trp Asn Ser Val Phe
385 390 395 400

Ser Gly Ile Ala Gly Ser Leu Asp Glu Leu Glu Ser Asp Ser His Phe
405 410 415

Cys Leu Asp Leu Ser Phe Gln Val Ser Leu Leu His Thr Gly Tyr Asp

420

36120A Suppl SL
425

430

Ile Pro Leu Gln Arg Glu Leu Arg Thr Gly Lys Lys Ile Ala Asn Lys
 435 440 445

Glu Ile Gly Trp Cys Leu Gly Ala Ser Leu Pro Leu Leu Lys Ala Asp
 450 455 460

Asn Trp Lys Cys Lys Ile Gln Ser Ala
 465 470

<210> 13

<211> 153

<212> PRT

<213> Homo sapiens

<400> 13

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
 1 5 10 15

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
 20 25 30

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
 35 40 45

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
 50 55 60

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
 65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
 85 90 95

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
 100 105 110

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
 115 120 125

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
 130 135 140

Lys Thr Arg Trp Phe Ser Ile Val Pro
145 150

<210> 14

<211> 154

<212> PRT

<213> Rattus norvegicus

<400> 14

Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Asn Leu
1 5 10 15

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
20 25 30

Gln Leu Leu Glu Glu Cys Gln Val Lys Gly Pro Gly Ile Ser Lys Tyr
35 40 45

Ala Gln Lys Thr Asp Glu Ile Ala Ala Tyr Leu Ala Glu Cys Met Lys
50 55 60

Met Ser Thr Glu Arg Ile Pro Ala Ser Lys Gln His Gln Thr Pro Val
65 70 75 80

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Lys
85 90 95

Gln Ser Ala Asp Glu Val Leu Ala Ala Val Ser Arg Ser Leu Lys Ser
100 105 110

Tyr Pro Phe Asp Phe Gln Gly Ala Lys Ile Ile Thr Gly Gln Glu Glu
115 120 125

Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Arg Phe Thr
130 135 140

Gln Glu Gln Ser Trp Leu Asn Phe Ile Ser
145 150

<210> 15

<211> 153

<212> PRT

<213> Homo sapiens

36120A suppl SL

<400> 15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Met Phe
1 5 10 15

Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Ile Val Gly
20 25 30

Gln His Ser Ser Cys Asp Val Pro Gly Gly Gly Ile Ser Ser Tyr Ala
35 40 45

Asp Asn Pro Ser Gly Ala Ser Gln Ser Leu Val Gly Cys Leu Glu Gln
50 55 60

Ala Leu Gln Asp Val Pro Lys Glu Arg His Ala Gly Thr Pro Leu Tyr
65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Asn Leu Thr Asn Pro Glu
85 90 95

Ala Ser Thr Ser Val Leu Met Ala Val Thr His Thr Leu Thr Gln Tyr
100 105 110

Pro Phe Asp Phe Arg Gly Ala Arg Ile Leu Ser Gly Gln Glu Glu Gly
115 120 125

Val Phe Gly Trp Val Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
130 135 140

Tyr Gly Trp Val Gly Arg Trp Phe Arg
145 150

<210> 16

<211> 150

<212> PRT

<213> Gallus gallus

<400> 16

Phe Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ala Val
1 5 10 15

Phe Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Val Val
20 25 30

36120A Suppl SL

Ser Glu His Ser Met Cys Asp Val Glu Gly Pro Gly Ile Ser Ser Tyr
35 40 45

Ser Ser Lys Pro Pro Ala Ala Gly Lys Ser Leu Glu His Cys Leu Ser
50 55 60

Gln Ala Met Arg Asp Val Pro Lys Glu Lys His Ala Asp Thr Pro Leu
65 70 75 80

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Thr Ile Ala Asp Pro
85 90 95

Pro Ser Gln Thr Cys Leu Ser Ala Val Met Ala Thr Leu Lys Ser Tyr
100 105 110

Pro Phe Asp Phe Gly Gly Ala Lys Ile Leu Ser Gly Glu Glu Glu Gly
115 120 125

Val Phe Gly Trp Ile Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
130 135 140

Arg Gly Trp Leu Gly Glu
145 150

<210> 17

<211> 148

<212> PRT

<213> Caenorhabditis elegans

<400> 17

Ile Lys Tyr Gly Val Ile Cys Asp Ala Gly Ser Ser Gly Thr Arg Leu
1 5 10 15

Phe Val Tyr Thr Leu Lys Pro Leu Ser Gly Gly Leu Thr Asn Ile Asp
20 25 30

Thr Leu Ile His Glu Ser Glu Pro Val Val Lys Lys Val Thr Pro Gly
35 40 45

Leu Ser Ser Phe Gly Asp Lys Pro Glu Gln Val Val Glu Tyr Leu Thr
50 55 60

Pro Leu Leu Arg Phe Ala Glu Glu His Ile Pro Tyr Glu Gln Leu Gly
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65

70

75

80

Glu Thr Asp Leu Leu Ile Phe Ala Thr Ala Gly Met Arg Leu Leu Pro
 85 90 95

Glu Ala Gln Lys Asp Ala Ile Ile Lys Asn Leu Gln Asn Gly Leu Lys
 100 105 110

Ser Val Thr Ala Leu Arg Val Ser Asp Ser Asn Ile Arg Ile Ile Asp
 115 120 125

Gly Ala Trp Glu Gly Ile Tyr Ser Trp Ile Ala Val Asn Tyr Ile Leu
 130 135 140

Gly Arg Phe Asp
 145

<210> 18

<211> 10

<212> RNA

<213> Mus musculus

<400> 18
 aagaauaugg

10

<210> 19

<211> 10

<212> RNA

<213> vertebrate

<400> 19
 gccgccaugg

10

<210> 20

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 20

ccagactgta aatcttttgg

20

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 21

aggggaatgta ataagggtag

20

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 22

ctgcttgagt gacgtctctg

20

<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 23

cacatgaggt tcagctcgtg

20

<210> 24

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 24
gtgaagtggc tgccttcagg

20

<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 25
cctttgactc gggactccag

20

<210> 26

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<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 26
gaactgctgc ctaaccactc

20

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 27
attgatgggt cttgggattg c 21

<210> 28

<211> 10

<212> RNA

<213> Homo sapiens

<400> 28
augugauga 10

<210> 29

<211> 10

<212> RNA

<213> Homo sapiens

<400> 29
acaaggauga 10

<210> 30

<211> 6

<212> RNA

<213> Homo sapiens

<400> 30
aauaaa 6

<210> 31

<211> 20

<212> DNA

<213> Homo sapiens

<400> 31
caggtcactt atggagcctg 20

<210> 32

36120A suppl SL

<211> 18

<212> DNA

<213> Homo sapiens

<400> 32
ccatggacaa aataggac

18